

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Chambon, Pierre
Gronemeyer, Hinrich
Voegel, Johannes
Lutz, Yves
- (ii) TITLE OF INVENTION: Transcriptional Intermediary Factor-2
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
(B) STREET: 1100 New York Avenue, NW, Suite 600
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/021,247
(B) FILING DATE: 12-JUL-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Steffe, Eric K.
(B) REGISTRATION NUMBER: 36,688
(C) REFERENCE/DOCKET NUMBER: 1383.0130001/EKS
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-371-2600
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

004255 042601
109240 922436

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 163..4554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCGGCCGCA GCCTCGGCTA CAGCTTCGGC GGCGAAGGTC AGCGCCGACG GCAGCCGGCA	60
CCTGACGGCG TGACCGACCC GAGCCGATTT CTCTTGGATT TGGCTACACA CTTATAGATC	120
TTCTGCACTG TTTACAGGCA CAGTTGCTGA TATGTGTTCA AG ATG AGT GGG ATG	174
Met Ser Gly Met	
1	
GGA GAA AAT ACC TCT GAC CCC TCC AGG GCA GAG ACA AGA AAG CGC AAG	222
Gly Glu Asn Thr Ser Asp Pro Ser Arg Ala Glu Thr Arg Lys Arg Lys	
5 10 15 20	
GAA TGT CCT GAC CAA CTT GGA CCC AGC CCC AAA AGG AAC ACT GAA AAA	270
Glu Cys Pro Asp Gln Leu Gly Pro Ser Pro Lys Arg Asn Thr Glu Lys	
25 30 35	
CGT AAT CGT GAA CAG GAA AAT AAA TAT ATA GAA GAA CTT GCA GAG TTG	318
Arg Asn Arg Glu Gln Glu Asn Lys Tyr Ile Glu Glu Leu Ala Glu Leu	
40 45 50	
ATT TTT GCA AAT TTT AAT GAT ATA GAC AAC TTT AAC TTC AAA CCT GAC	366
Ile Phe Ala Asn Phe Asn Asp Ile Asp Asn Phe Asn Phe Lys Pro Asp	
55 60 65	
AAA TGT GCA ATC TTA AAA GAA ACT GTG AAG CAA ATT CGT CAG ATC AAA	414
Lys Cys Ala Ile Leu Lys Glu Thr Val Lys Gln Ile Arg Gln Ile Lys	
70 75 80	
GAA CAA GAG AAA GCA GCA GCT GCC AAC ATA GAT GAA GTG CAG AAG TCA	462
Glu Gln Glu Lys Ala Ala Ala Ala Asn Ile Asp Glu Val Gln Lys Ser	
85 90 95 100	
GAT GTA TCC TCT ACA GGG CAG GGT GTC ATC GAC AAG GAT GCG CTG GGG	510
Asp Val Ser Ser Thr Gly Gln Gly Val Ile Asp Lys Asp Ala Leu Gly	
105 110 115	
CCT ATG ATG CTT GAG GCC CTT GAT GGG TTC TTC TTT GTA GTG AAC CTG	558
Pro Met Met Leu Glu Ala Leu Asp Gly Phe Phe Phe Val Val Asn Leu	
120 125 130	
GAA GGC AAC GTT GTG TTT GTG TCA GAG AAT GTG ACA CAG TAT CTA AGG	606
Glu Gly Asn Val Val Phe Val Ser Glu Asn Val Thr Gln Tyr Leu Arg	
135 140 145	
TAT AAC CAA GAA GAG CTG ATG AAC AAA AGT GTA TAT AGC ATC TTG CAT	654
Tyr Asn Gln Glu Glu Leu Met Asn Lys Ser Val Tyr Ser Ile Leu His	
150 155 160	
GTT GGG GAC CAC ACG GAA TTT GTC AAA AAC CTG CTG CCA AAG TCT ATA	702
Val Gly Asp His Thr Glu Phe Val Lys Asn Leu Leu Pro Lys Ser Ile	

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165	170	175	180	
GTA AAT GGG GGA TCT TGG TCT GGC GAA CCT CCG AGG CGG AAC AGC CAT				750
Val Asn Gly Gly Ser Trp Ser Gly Glu Pro Pro Arg Arg Asn Ser His	185	190	195	
ACC TTC AAT TGT CGG ATG CTG GTA AAA CCT TTA CCT GAT TCA GAA GAG				798
Thr Phe Asn Cys Arg Met Leu Val Lys Pro Leu Pro Asp Ser Glu Glu	200	205	210	
GAG GGT CAT GAT AAC CAG GAA GCT CAT CAG AAA TAT GAA ACT ATG CAG				846
Glu Gly His Asp Asn Gln Glu Ala His Gln Lys Tyr Glu Thr Met Gln	215	220	225	
TGC TTC GCT GTC TCT CAA CCA AAG TCC ATC AAA GAA GAA GGA GAA GAT				894
Cys Phe Ala Val Ser Gln Pro Lys Ser Ile Lys Glu Glu Gly Glu Asp	230	235	240	
TTG CAG TCC TGC TTG ATT TGC GTG GCA AGA AGA GTT CCC ATG AAG GAA				942
Leu Gln Ser Cys Leu Ile Cys Val Ala Arg Arg Val Pro Met Lys Glu	245	250	255	260
AGA CCA GTT CTT CCC TCA TCA GAA AGT TTT ACT ACT CGC CAG GAT CTC				990
Arg Pro Val Leu Pro Ser Ser Glu Ser Phe Thr Thr Arg Gln Asp Leu	265	270	275	
CAA GGC AAG ATC ACG TCT CTG GAT ACC AGC ACC ATG AGA GCA GCC ATG				1038
Gln Gly Lys Ile Thr Ser Leu Asp Thr Ser Thr Met Arg Ala Ala Met	280	285	290	
AAA CCA GGC TGG GAG GAC CTG GTA AGA AGG TGT ATT CAG AAG TTC CAT				1086
Lys Pro Gly Trp Glu Asp Leu Val Arg Arg Cys Ile Gln Lys Phe His	295	300	305	
GCG CAG CAT GAA GGA GAA TCT GTG TCC TAT GCT AAG AGG CAT CAT CAT				1134
Ala Gln His Glu Gly Glu Ser Val Ser Tyr Ala Lys Arg His His His	310	315	320	
GAA GTA CTG AGA CAA GGA TTG GCA TTC AGT CAA ATC TAT CGT TTT TCC				1182
Glu Val Leu Arg Gln Gly Leu Ala Phe Ser Gln Ile Tyr Arg Phe Ser	325	330	335	340
TTG TCT GAT GGC ACT CTT GTT GCT GCA CAA ACG AAG AGC AAA CTC ATC				1230
Leu Ser Asp Gly Thr Leu Val Ala Ala Gln Thr Lys Ser Lys Leu Ile	345	350	355	
CGT TCT CAG ACT ACT AAT GAA CCT CAA CTT GTA ATA TCT TTA CAT ATG				1278
Arg Ser Gln Thr Thr Asn Glu Pro Gln Leu Val Ile Ser Leu His Met	360	365	370	
CTT CAC AGA GAG CAG AAT GTG TGT GTG ATG AAT CCG GAT CTG ACT GGA				1326
Leu His Arg Glu Gln Asn Val Cys Val Met Asn Pro Asp Leu Thr Gly	375	380	385	
CAA ACG ATG GGG AAG CCA CTG AAT CCA ATT AGC TCT AAC AGC CCT GCC				1374
Gln Thr Met Gly Lys Pro Leu Asn Pro Ile Ser Ser Asn Ser Pro Ala	390	395	400	

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CAT CAG GCC CTG TGC AGT GGG AAC CCA GGT CAG GAC ATG ACC CTC AGT His Gln Ala Leu Cys Ser Gly Asn Pro Gly Gln Asp Met Thr Leu Ser 405 410 415 420	1422
AGC AAT ATA AAT TTT CCC ATA AAT GGC CCA AAG GAA CAA ATG GGC ATG Ser Asn Ile Asn Phe Pro Ile Asn Gly Pro Lys Glu Gln Met Gly Met 425 430 435	1470
CCC ATG GGC AGG TTT GGT GGT TCT GGG GGA ATG AAC CAT GTG TCA GGC Pro Met Gly Arg Phe Gly Gly Ser Gly Gly Met Asn His Val Ser Gly 440 445 450	1518
ATG CAA GCA ACC ACT CCT CAG GGT AGT AAC TAT GCA CTC AAA ATG AAC Met Gln Ala Thr Thr Pro Gln Gly Ser Asn Tyr Ala Leu Lys Met Asn 455 460 465	1566
AGC CCC TCA CAA AGC AGC CCT GGC ATG AAT CCA GGA CAG CCC ACC TCC Ser Pro Ser Gln Ser Ser Pro Gly Met Asn Pro Gly Gln Pro Thr Ser 470 475 480	1614
ATG CTT TCA CCA AGG CAT CGC ATG AGC CCT GGA GTG GCT GGC AGC CCT Met Leu Ser Pro Arg His Arg Met Ser Pro Gly Val Ala Gly Ser Pro 485 490 495 500	1662
CGA ATC CCA CCC AGT CAG TTT TCC CCT GCA GGA AGC TTG CAT TCC CCT Arg Ile Pro Pro Ser Gln Phe Ser Pro Ala Gly Ser Leu His Ser Pro 505 510 515	1710
GTG GGA GTT TGC AGC AGC ACA GGA AAT AGC CAT AGT TAT ACC AAC AGC Val Gly Val Cys Ser Ser Thr Gly Asn Ser His Ser Tyr Thr Asn Ser 520 525 530	1758
TCC CTC AAT GCA CTT CAG GCC CTC AGC GAG GGG CAC GGG GTC TCA TTA Ser Leu Asn Ala Leu Gln Ala Leu Ser Glu Gly His Gly Val Ser Leu 535 540 545	1806
GGG TCA TCG TTG GCT TCA CCA GAC CTA AAA ATG GGC AAT TTG CAA AAC Gly Ser Ser Leu Ala Ser Pro Asp Leu Lys Met Gly Asn Leu Gln Asn 550 555 560	1854
TCC CCA GTT AAT ATG AAT CCT CCC CCA CTC AGC AAG ATG GGA AGC TTG Ser Pro Val Asn Met Asn Pro Pro Pro Leu Ser Lys Met Gly Ser Leu 565 570 575 580	1902
GAC TCA AAA GAC TGT TTT GGA CTA TAT GGG GAG CCC TCT GAA GGT ACA Asp Ser Lys Asp Cys Phe Gly Leu Tyr Gly Glu Pro Ser Glu Gly Thr 585 590 595	1950
ACT GGA CAA GCA GAG AGC AGC TGC CAT CCT GGA GAG CAA AAG GAA ACA Thr Gly Gln Ala Glu Ser Ser Cys His Pro Gly Glu Gln Lys Glu Thr 600 605 610	1998
AAT GAC CCC AAC CTG CCC CCG GCC GTG AGC AGT GAG AGA GCT GAC GGG Asn Asp Pro Asn Leu Pro Pro Ala Val Ser Ser Glu Arg Ala Asp Gly 615 620 625	2046
CAG AGC AGA CTG CAT GAC AGC AAA GGG CAG ACC AAA CTC CTG CAG CTG	2094

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Gln	Ser	Arg	Leu	His	Asp	Ser	Lys	Gly	Gln	Thr	Lys	Leu	Leu	Gln	Leu		
630						635					640						
CTG	ACC	ACC	AAA	TCT	GAT	CAG	ATG	GAG	CCC	TCG	CCC	TTA	GCC	AGC	TCT	2142	
Leu	Thr	Thr	Lys	Ser	Asp	Gln	Met	Glu	Pro	Ser	Pro	Leu	Ala	Ser	Ser		
645					650					655					660		
TTG	TCG	GAT	ACA	AAC	AAA	GAC	TCC	ACA	GGT	AGC	TTG	CCT	GGT	TCT	GGG	2190	
Leu	Ser	Asp	Thr	Asn	Lys	Asp	Ser	Thr	Gly	Ser	Leu	Pro	Gly	Ser	Gly		
				665					670					675			
TCT	ACA	CAT	GGA	ACC	TCG	CTC	AAG	GAG	AAG	CAT	AAA	ATT	TTG	CAC	AGA	2238	
Ser	Thr	His	Gly	Thr	Ser	Leu	Lys	Glu	Lys	His	Lys	Ile	Leu	His	Arg		
			680					685					690				
CTC	TTG	CAG	GAC	AGC	AGT	TCC	CCT	GTG	GAC	TTG	GCC	AAG	TTA	ACA	GCA	2286	
Leu	Leu	Gln	Asp	Ser	Ser	Ser	Pro	Val	Asp	Leu	Ala	Lys	Leu	Thr	Ala		
		695					700					705					
GAA	GCC	ACA	GGC	AAA	GAC	CTG	AGC	CAG	GAG	TCC	AGC	AGC	ACA	GCT	CCT	2334	
Glu	Ala	Thr	Gly	Lys	Asp	Leu	Ser	Gln	Glu	Ser	Ser	Ser	Thr	Ala	Pro		
	710					715					720						
GGA	TCA	GAA	GTG	ACT	ATT	AAA	CAA	GAG	CCG	GTG	AGC	CCC	AAG	AAG	AAA	2382	
Gly	Ser	Glu	Val	Thr	Ile	Lys	Gln	Glu	Pro	Val	Ser	Pro	Lys	Lys	Lys		
725					730				735						740		
GAG	AAT	GCA	CTA	CTT	CGC	TAT	TTG	CTA	GAT	AAA	GAT	GAT	ACT	AAA	GAT	2430	
Glu	Asn	Ala	Leu	Leu	Arg	Tyr	Leu	Leu	Asp	Lys	Asp	Asp	Thr	Lys	Asp		
				745					750					755			
ATT	GGT	TTA	CCA	GAA	ATA	ACC	CCC	AAA	CTT	GAG	AGA	CTG	GAC	AGT	AAG	2478	
Ile	Gly	Leu	Pro	Glu	Ile	Thr	Pro	Lys	Leu	Glu	Arg	Leu	Asp	Ser	Lys		
			760					765					770				
ACA	GAT	CCT	GCC	AGT	AAC	ACA	AAA	TTA	ATA	GCA	ATG	AAA	ACT	GAG	AAG	2526	
Thr	Asp	Pro	Ala	Ser	Asn	Thr	Lys	Leu	Ile	Ala	Met	Lys	Thr	Glu	Lys		
		775					780					785					
GAG	GAG	ATG	AGC	TTT	GAG	CCT	GGT	GAC	CAG	CCT	GGC	AGT	GAG	CTG	GAC	2574	
Glu	Glu	Met	Ser	Phe	Glu	Pro	Gly	Asp	Gln	Pro	Gly	Ser	Glu	Leu	Asp		
	790					795					800						
AAC	TTG	GAG	GAG	ATT	TTG	GAT	GAT	TTG	CAG	AAT	AGT	CAA	TTA	CCA	CAG	2622	
Asn	Leu	Glu	Glu	Ile	Leu	Asp	Asp	Leu	Gln	Asn	Ser	Gln	Leu	Pro	Gln		
805					810					815					820		
CTT	TTC	CCA	GAC	ACG	AGG	CCA	GGC	GCC	CCT	GCT	GGA	TCA	GTT	GAC	AAG	2670	
Leu	Phe	Pro	Asp	Thr	Arg	Pro	Gly	Ala	Pro	Ala	Gly	Ser	Val	Asp	Lys		
				825					830					835			
CAA	GCC	ATC	ATC	AAT	GAC	CTC	ATG	CAA	CTC	ACA	GCT	GAA	AAC	AGC	CCT	2718	
Gln	Ala	Ile	Ile	Asn	Asp	Leu	Met	Gln	Leu	Thr	Ala	Glu	Asn	Ser	Pro		
			840					845					850				
GTC	ACA	CCT	GTT	GGA	GCC	CAG	AAA	ACA	GCA	CTG	CGA	ATT	TCA	CAG	AGC	2766	
Val	Thr	Pro	Val	Gly	Ala	Gln	Lys	Thr	Ala	Leu	Arg	Ile	Ser	Gln	Ser		

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855	860	865	
ACT TTT AAT AAC CCA CGA CCA GGG CAA CTG GGC AGG TTA TTG CCA AAC Thr Phe Asn Asn Pro Arg Pro Gly Gln Leu Gly Arg Leu Leu Pro Asn 870 875 880			2814
CAG AAT TTA CCA CTT GAC ATC ACA TTG CAA AGC CCA ACT GGT GCT GGA Gln Asn Leu Pro Leu Asp Ile Thr Leu Gln Ser Pro Thr Gly Ala Gly 885 890 895 900			2862
CCT TTC CCA CCA ATC AGA AAC AGT AGT CCC TAC TCA GTG ATA CCT CAG Pro Phe Pro Pro Ile Arg Asn Ser Ser Pro Tyr Ser Val Ile Pro Gln 905 910 915			2910
CCA GGA ATG ATG GGT AAT CAA GGG ATG ATA GGA AAC CAA GGA AAT TTA Pro Gly Met Met Gly Asn Gln Gly Met Ile Gly Asn Gln Gly Asn Leu 920 925 930			2958
GGG AAC AGT AGC ACA GGA ATG ATT GGT AAC AGT GCT TCT CGG CCT ACT Gly Asn Ser Ser Thr Gly Met Ile Gly Asn Ser Ala Ser Arg Pro Thr 935 940 945			3006
ATG CCA TCT GGA GAA TGG GCA CCG CAG AGT TCG GCT GTG AGA GTC ACC Met Pro Ser Gly Glu Trp Ala Pro Gln Ser Ser Ala Val Arg Val Thr 950 955 960			3054
TGT GCT GCT ACC ACC AGT GCC ATG AAC CGG CCA GTC CAA GGA GGT ATG Cys Ala Ala Thr Thr Ser Ala Met Asn Arg Pro Val Gln Gly Gly Met 965 970 975 980			3102
ATT CGG AAC CCA GCA GCC AGC ATC CCC ATG AGG CCC AGC AGC CAG CCT Ile Arg Asn Pro Ala Ala Ser Ile Pro Met Arg Pro Ser Ser Gln Pro 985 990 995			3150
GGC CAA AGA CAG ACG CTT CAG TCT CAG GTC ATG AAT ATA GGG CCA TCT Gly Gln Arg Gln Thr Leu Gln Ser Gln Val Met Asn Ile Gly Pro Ser 1000 1005 1010			3198
GAA TTA GAG ATG AAC ATG GGG GGA CCT CAG TAT AGC CAA CAA CAA GCT Glu Leu Glu Met Asn Met Gly Gly Pro Gln Tyr Ser Gln Gln Gln Ala 1015 1020 1025			3246
CCT CCA AAT CAG ACT GCC CCA TGG CCT GAA AGC ATC CTG CCT ATA GAC Pro Pro Asn Gln Thr Ala Pro Trp Pro Glu Ser Ile Leu Pro Ile Asp 1030 1035 1040			3294
CAG GCG TCT TTT GCC AGC CAA AAC AGG CAG CCA TTT GGC AGT TCT CCA Gln Ala Ser Phe Ala Ser Gln Asn Arg Gln Pro Phe Gly Ser Ser Pro 1045 1050 1055 1060			3342
GAT GAC TTG CTA TGT CCA CAT CCT GCA GCT GAG TCT CCG AGT GAT GAG Asp Asp Leu Leu Cys Pro His Pro Ala Ala Glu Ser Pro Ser Asp Glu 1065 1070 1075			3390
GGA GCT CTC CTG GAC CAG CTG TAT CTG GCC TTG CGG AAT TTT GAT GGC Gly Ala Leu Leu Asp Gln Leu Tyr Leu Ala Leu Arg Asn Phe Asp Gly 1080 1085 1090			3438

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CTG GAG GAG ATT GAT AGA GCC TTA GGA ATA CCC GAA CTG GTC AGC CAG Leu Glu Glu Ile Asp Arg Ala Leu Gly Ile Pro Glu Leu Val Ser Gln 1095 1100 1105	3486
AGC CAA GCA GTA GAT CCA GAA CAG TTC TCA AGT CAG GAT TCC AAC ATC Ser Gln Ala Val Asp Pro Glu Gln Phe Ser Ser Gln Asp Ser Asn Ile 1110 1115 1120	3534
ATG CTG GAG CAG AAG GCG CCC GTT TTC CCA CAG CAG TAT GCA TCT CAG Met Leu Glu Gln Lys Ala Pro Val Phe Pro Gln Gln Tyr Ala Ser Gln 1125 1130 1135 1140	3582
GCA CAA ATG GCC CAG GGT AGC TAT TCT CCC ATG CAA GAT CCA AAC TTT Ala Gln Met Ala Gln Gly Ser Tyr Ser Pro Met Gln Asp Pro Asn Phe 1145 1150 1155	3630
CAC ACC ATG GGA CAG CGG CCT AGT TAT GCC ACA CTC CGT ATG CAG CCC His Thr Met Gly Gln Arg Pro Ser Tyr Ala Thr Leu Arg Met Gln Pro 1160 1165 1170	3678
AGA CCG GGC CTC AGG CCC ACG GGC CTA GTG CAG AAC CAG CCA AAT CAA Arg Pro Gly Leu Arg Pro Thr Gly Leu Val Gln Asn Gln Pro Asn Gln 1175 1180 1185	3726
CTA AGA CTT CAA CTT CAG CAT CGC CTC CAA GCA CAG CAG AAT CGC CAG Leu Arg Leu Gln Leu Gln His Arg Leu Gln Ala Gln Gln Asn Arg Gln 1190 1195 1200	3774
CCA CTT ATG AAT CAA ATC AGC AAT GTT TCC AAT GTG AAC TTG ACT CTG Pro Leu Met Asn Gln Ile Ser Asn Val Ser Asn Val Asn Leu Thr Leu 1205 1210 1215 1220	3822
AGG CCT GGA GTA CCA ACA CAG GCA CCT ATT AAT GCA CAG ATG CTG GCC Arg Pro Gly Val Pro Thr Gln Ala Pro Ile Asn Ala Gln Met Leu Ala 1225 1230 1235	3870
CAG AGA CAG AGG GAA ATC CTG AAC CAG CAT CTT CGA CAG AGA CAA ATG Gln Arg Gln Arg Glu Ile Leu Asn Gln His Leu Arg Gln Arg Gln Met 1240 1245 1250	3918
CAT CAG CAA CAG CAA GTT CAG CAA CGA ACT TTG ATG ATG AGA GGA CAA His Gln Gln Gln Gln Val Gln Gln Arg Thr Leu Met Met Arg Gly Gln 1255 1260 1265	3966
GGG TTG AAT ATG ACA CCA AGC ATG GTG GCT CCT AGT GGT ATG CCA GCA Gly Leu Asn Met Thr Pro Ser Met Val Ala Pro Ser Gly Met Pro Ala 1270 1275 1280	4014
ACT ATG AGC AAC CCT CGG ATT CCC CAG GCA AAT GCA CAG CAG TTT CCA Thr Met Ser Asn Pro Arg Ile Pro Gln Ala Asn Ala Gln Gln Phe Pro 1285 1290 1295 1300	4062
TTT CCT CCA AAC TAC GGA ATA AGT CAG CAA CCT GAT CCA GGC TTT ACT Phe Pro Pro Asn Tyr Gly Ile Ser Gln Gln Pro Asp Pro Gly Phe Thr 1305 1310 1315	4110
GGG GCT ACG ACT CCC CAG AGC CCA CTT ATG TCA CCC CGA ATG GCA CAT	4158

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Gly Ala Thr Thr Pro Gln Ser Pro Leu Met Ser Pro Arg Met Ala His	
1320 1325 1330	
ACA CAG AGT CCC ATG ATG CAA CAG TCT CAG GCC AAC CCA GCC TAT CAG	4206
Thr Gln Ser Pro Met Met Gln Gln Ser Gln Ala Asn Pro Ala Tyr Gln	
1335 1340 1345	
GCC CCC TCC GAC ATA AAT GGA TGG GCG CAG GGG AAC ATG GGC GGA AAC	4254
Ala Pro Ser Asp Ile Asn Gly Trp Ala Gln Gly Asn Met Gly Gly Asn	
1350 1355 1360	
AGC ATG TTT TCC CAG CAG TCC CCA CCA CAC TTT GGG CAG CAA GCA AAC	4302
Ser Met Phe Ser Gln Gln Ser Pro Pro His Phe Gly Gln Gln Ala Asn	
1365 1370 1375 1380	
ACC AGC ATG TAC AGT AAC AAC ATG AAC ATC AAT GTG TCC ATG GCG ACC	4350
Thr Ser Met Tyr Ser Asn Asn Met Asn Ile Asn Val Ser Met Ala Thr	
1385 1390 1395	
AAC ACA GGT GGC ATG AGC AGC ATG AAC CAG ATG ACA GGA CAG ATC AGC	4398
Asn Thr Gly Gly Met Ser Ser Met Asn Gln Met Thr Gly Gln Ile Ser	
1400 1405 1410	
ATG ACC TCA GTG ACC TCC GTG TCT ACG TCA GGG CTG TCC TCC ATG GGT	4446
Met Thr Ser Val Thr Ser Val Ser Thr Ser Gly Leu Ser Ser Met Gly	
1415 1420 1425	
CCC GAG CAG GTT AAT GAT CCT GCT CTG AGG GGA GGC AAC CTG TTC CCA	4494
Pro Glu Gln Val Asn Asp Pro Ala Leu Arg Gly Gly Asn Leu Phe Pro	
1430 1435 1440	
AAC CAG CTG CCT GGA ATG GAT ATG ATT AAG CAG GAG GGA GAC ACA ACA	4542
Asn Gln Leu Pro Gly Met Asp Met Ile Lys Gln Glu Gly Asp Thr Thr	
1445 1450 1455 1460	
CGG AAA TAT TGC TGACACTGCT GAAGCCAGTT GCTTCTTCAG CTGACCGGGC	4594
Arg Lys Tyr Cys	
TCACCTGCTC AAAACACTTC CAGTCTGGAG AGCTGTGTCT ATTTGTTTCA ACCCAACTGA	4654
CCTGCCAGCC GGTTCTGCTA GAGCAGACAG GCCTGGCCCT GGTTCCCAGG GTGGCGTCCA	4714
CTCGGCTGTG GCAGGAGGAG CTGCCTCTTC TCTTGACAGT CTGAAGCTCG CATCCAGACA	4774
GTCGCTCAGT CTGTTCCCTG CATTACCTT AGTGCAACTT AGATCTCTCC TCCCCAAGTA	4834
AATGTTGACA GGCCAATTTC ATACCCATGT CAGATTGAAT GTATTTAAAT GTATGTATTT	4894
AAGGAGAACC ATGCTCTTGT TCTGTTCCCTG TTCGGTTCCA GACACTGGTT TCTTGCTTTG	4954
TTTTCCCTGG CTAACAGTCT AGTGCCAAAG ATTAAGATTT TATCTGGGGG AAAGAAAAGA	5014
ATTTTTTAAA AAATTAACT AAAGATGTTT TAAGCTAAAG CCTGAATTTG GGATGGAAGC	5074
AGGACAGACA CCGTGGACAG CGCTGTATTT ACAGACACAC CCAGTGCGTG AAGACCAACA	5134

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AAGTCACAGT CGTATCTCTA GAAAGCTCTA AAGACCATGT TGGAAAGAGT CTCCAGTTAC 5194
TGAACAGATG AAAAGGAGCC TGTGAGAGGG CTGTTAACAT TAGCAAATAT TTTTTCCTTG 5254
TTTTTCTTT GTTAAACCA AACTGGTTCA CCTGAATCAT GAATTGAGAA GAAATAATTT 5314
TCATTTCTAA ATTAAGTCCC TTTTAGTTTG ATCAGACAGC TTGAATCAGC ATCTCTTCTT 5374
CCCTGTCAGC CTGACTCTTC CTTTCCCCTC TCTCATTTCC CATACTCCCT ATTTTCATTC 5434
CTTTTTTAAA AAATAATATA AGCTACAGAA ACCAGGTAAG CCCTTTATTT CCTTAAATGT 5494
TTTGCCAGCC ACTTACCAAT TGCTAAGTAT TGAATTTTCA AAAAAAAAAA TGCATTTACT 5554
GGCAAGGAGA AGAGCAAAGT TAAGGCTTGA TACCAATCGA GCTAAGGATA CCTGCTTTGG 5614
AAGCATGTTT ATTCTGTTCC CCAGCAACTC TGGCCTCCAA AATGGGAGAA ACGCCAGTGT 5674
GTTTAAATTG ATAGCAGATA TCACGACAGA TTTAACCTCT GCCATGTGTT TTTTATTTTG 5734
TTTTTTAGCA GTGCTGACTA AGCCGAAGTT TTGTAAGGTA CATAAAATCC AATTTATATG 5794
TAAACAAGCA ATAATTTAAG TTGAGAACTT ATGTGTTTTA ATTGTATAAT TTTTGTGAGG 5854
TATACATATT GTGGAATTGA CTCAAAATG AGGTACTTCA GTATTAAATT AGATATCTTC 5914
ATAGCAATGT CTCCTAAAGG TGTTTTGTAA AGGATATCAA TGCCTTGATT AGACCTAATT 5974
TGTAGACTTA AGACTTTTTA TTTTCTAAAC CTTGTGATTC TGCTTATAAG TCATTTATCT 6034
AATCTATATG ATATGCAGCC GCTGTAGGAA CCAATTCTTG ATTTTATATAT GTTTATATTC 6094
TTTCTTAATG AACCTTAGAA AGACTACATG TTTACTAAGCA GGCCACTTTT ATGGTTGTTT 6154
TT 6156

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1464 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Gly Met Gly Glu Asn Thr Ser Asp Pro Ser Arg Ala Glu Thr
1 5 10 15
Arg Lys Arg Lys Glu Cys Pro Asp Gln Leu Gly Pro Ser Pro Lys Arg
20 25 30
Asn Thr Glu Lys Arg Asn Arg Glu Gln Glu Asn Lys Tyr Ile Glu Glu
35 40 45

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Leu Ala Glu Leu Ile Phe Ala Asn Phe Asn Asp Ile Asp Asn Phe Asn
 50 55 60
 Phe Lys Pro Asp Lys Cys Ala Ile Leu Lys Glu Thr Val Lys Gln Ile
 65 70 75 80
 Arg Gln Ile Lys Glu Gln Glu Lys Ala Ala Ala Ala Asn Ile Asp Glu
 85 90 95
 Val Gln Lys Ser Asp Val Ser Ser Thr Gly Gln Gly Val Ile Asp Lys
 100 105 110
 Asp Ala Leu Gly Pro Met Met Leu Glu Ala Leu Asp Gly Phe Phe Phe
 115 120 125
 Val Val Asn Leu Glu Gly Asn Val Val Phe Val Ser Glu Asn Val Thr
 130 135 140
 Gln Tyr Leu Arg Tyr Asn Gln Glu Glu Leu Met Asn Lys Ser Val Tyr
 145 150 155 160
 Ser Ile Leu His Val Gly Asp His Thr Glu Phe Val Lys Asn Leu Leu
 165 170 175
 Pro Lys Ser Ile Val Asn Gly Gly Ser Trp Ser Gly Glu Pro Pro Arg
 180 185 190
 Arg Asn Ser His Thr Phe Asn Cys Arg Met Leu Val Lys Pro Leu Pro
 195 200 205
 Asp Ser Glu Glu Glu Gly His Asp Asn Gln Glu Ala His Gln Lys Tyr
 210 215 220
 Glu Thr Met Gln Cys Phe Ala Val Ser Gln Pro Lys Ser Ile Lys Glu
 225 230 235 240
 Glu Gly Glu Asp Leu Gln Ser Cys Leu Ile Cys Val Ala Arg Arg Val
 245 250 255
 Pro Met Lys Glu Arg Pro Val Leu Pro Ser Ser Glu Ser Phe Thr Thr
 260 265 270
 Arg Gln Asp Leu Gln Gly Lys Ile Thr Ser Leu Asp Thr Ser Thr Met
 275 280 285
 Arg Ala Ala Met Lys Pro Gly Trp Glu Asp Leu Val Arg Arg Cys Ile
 290 295 300
 Gln Lys Phe His Ala Gln His Glu Gly Glu Ser Val Ser Tyr Ala Lys
 305 310 315 320
 Arg His His His Glu Val Leu Arg Gln Gly Leu Ala Phe Ser Gln Ile
 325 330 335
 Tyr Arg Phe Ser Leu Ser Asp Gly Thr Leu Val Ala Ala Gln Thr Lys
 340 345 350

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Ser Lys Leu Ile Arg Ser Gln Thr Thr Asn Glu Pro Gln Leu Val Ile
355 360 365

Ser Leu His Met Leu His Arg Glu Gln Asn Val Cys Val Met Asn Pro
370 375 380

Asp Leu Thr Gly Gln Thr Met Gly Lys Pro Leu Asn Pro Ile Ser Ser
385 390 395 400

Asn Ser Pro Ala His Gln Ala Leu Cys Ser Gly Asn Pro Gly Gln Asp
405 410 415

Met Thr Leu Ser Ser Asn Ile Asn Phe Pro Ile Asn Gly Pro Lys Glu
420 425 430

Gln Met Gly Met Pro Met Gly Arg Phe Gly Gly Ser Gly Gly Met Asn
435 440 445

His Val Ser Gly Met Gln Ala Thr Thr Pro Gln Gly Ser Asn Tyr Ala
450 455 460

Leu Lys Met Asn Ser Pro Ser Gln Ser Ser Pro Gly Met Asn Pro Gly
465 470 475 480

Gln Pro Thr Ser Met Leu Ser Pro Arg His Arg Met Ser Pro Gly Val
485 490 495

Ala Gly Ser Pro Arg Ile Pro Pro Ser Gln Phe Ser Pro Ala Gly Ser
500 505 510

Leu His Ser Pro Val Gly Val Cys Ser Ser Thr Gly Asn Ser His Ser
515 520 525

Tyr Thr Asn Ser Ser Leu Asn Ala Leu Gln Ala Leu Ser Glu Gly His
530 535 540

Gly Val Ser Leu Gly Ser Ser Leu Ala Ser Pro Asp Leu Lys Met Gly
545 550 555 560

Asn Leu Gln Asn Ser Pro Val Asn Met Asn Pro Pro Pro Leu Ser Lys
565 570 575

Met Gly Ser Leu Asp Ser Lys Asp Cys Phe Gly Leu Tyr Gly Glu Pro
580 585 590

Ser Glu Gly Thr Thr Gly Gln Ala Glu Ser Ser Cys His Pro Gly Glu
595 600 605

Gln Lys Glu Thr Asn Asp Pro Asn Leu Pro Pro Ala Val Ser Ser Glu
610 615 620

Arg Ala Asp Gly Gln Ser Arg Leu His Asp Ser Lys Gly Gln Thr Lys
625 630 635 640

Leu Leu Gln Leu Leu Thr Thr Lys Ser Asp Gln Met Glu Pro Ser Pro
645 650 655

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Leu Ala Ser Ser Leu Ser Asp Thr Asn Lys Asp Ser Thr Gly Ser Leu
660 665 670

Pro Gly Ser Gly Ser Thr His Gly Thr Ser Leu Lys Glu Lys His Lys
675 680 685

Ile Leu His Arg Leu Leu Gln Asp Ser Ser Ser Pro Val Asp Leu Ala
690 695 700

Lys Leu Thr Ala Glu Ala Thr Gly Lys Asp Leu Ser Gln Glu Ser Ser
705 710 715 720

Ser Thr Ala Pro Gly Ser Glu Val Thr Ile Lys Gln Glu Pro Val Ser
725 730 735

Pro Lys Lys Lys Glu Asn Ala Leu Leu Arg Tyr Leu Leu Asp Lys Asp
740 745 750

Asp Thr Lys Asp Ile Gly Leu Pro Glu Ile Thr Pro Lys Leu Glu Arg
755 760 765

Leu Asp Ser Lys Thr Asp Pro Ala Ser Asn Thr Lys Leu Ile Ala Met
770 775 780

Lys Thr Glu Lys Glu Glu Met Ser Phe Glu Pro Gly Asp Gln Pro Gly
785 790 795 800

Ser Glu Leu Asp Asn Leu Glu Glu Ile Leu Asp Asp Leu Gln Asn Ser
805 810 815

Gln Leu Pro Gln Leu Phe Pro Asp Thr Arg Pro Gly Ala Pro Ala Gly
820 825 830

Ser Val Asp Lys Gln Ala Ile Ile Asn Asp Leu Met Gln Leu Thr Ala
835 840 845

Glu Asn Ser Pro Val Thr Pro Val Gly Ala Gln Lys Thr Ala Leu Arg
850 855 860

Ile Ser Gln Ser Thr Phe Asn Asn Pro Arg Pro Gly Gln Leu Gly Arg
865 870 875 880

Leu Leu Pro Asn Gln Asn Leu Pro Leu Asp Ile Thr Leu Gln Ser Pro
885 890 895

Thr Gly Ala Gly Pro Phe Pro Pro Ile Arg Asn Ser Ser Pro Tyr Ser
900 905 910

Val Ile Pro Gln Pro Gly Met Met Gly Asn Gln Gly Met Ile Gly Asn
915 920 925

Gln Gly Asn Leu Gly Asn Ser Ser Thr Gly Met Ile Gly Asn Ser Ala
930 935 940

Ser Arg Pro Thr Met Pro Ser Gly Glu Trp Ala Pro Gln Ser Ser Ala
945 950 955 960

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Val Arg Val Thr Cys Ala Ala Thr Thr Ser Ala Met Asn Arg Pro Val
965 970 975

Gln Gly Gly Met Ile Arg Asn Pro Ala Ala Ser Ile Pro Met Arg Pro
980 985 990

Ser Ser Gln Pro Gly Gln Arg Gln Thr Leu Gln Ser Gln Val Met Asn
995 1000 1005

Ile Gly Pro Ser Glu Leu Glu Met Asn Met Gly Gly Pro Gln Tyr Ser
1010 1015 1020

Gln Gln Gln Ala Pro Pro Asn Gln Thr Ala Pro Trp Pro Glu Ser Ile
1025 1030 1035 1040

Leu Pro Ile Asp Gln Ala Ser Phe Ala Ser Gln Asn Arg Gln Pro Phe
1045 1050 1055

Gly Ser Ser Pro Asp Asp Leu Leu Cys Pro His Pro Ala Ala Glu Ser
1060 1065 1070

Pro Ser Asp Glu Gly Ala Leu Leu Asp Gln Leu Tyr Leu Ala Leu Arg
1075 1080 1085

Asn Phe Asp Gly Leu Glu Glu Ile Asp Arg Ala Leu Gly Ile Pro Glu
1090 1095 1100

Leu Val Ser Gln Ser Gln Ala Val Asp Pro Glu Gln Phe Ser Ser Gln
1105 1110 1115 1120

Asp Ser Asn Ile Met Leu Glu Gln Lys Ala Pro Val Phe Pro Gln Gln
1125 1130 1135

Tyr Ala Ser Gln Ala Gln Met Ala Gln Gly Ser Tyr Ser Pro Met Gln
1140 1145 1150

Asp Pro Asn Phe His Thr Met Gly Gln Arg Pro Ser Tyr Ala Thr Leu
1155 1160 1165

Arg Met Gln Pro Arg Pro Gly Leu Arg Pro Thr Gly Leu Val Gln Asn
1170 1175 1180

Gln Pro Asn Gln Leu Arg Leu Gln Leu Gln His Arg Leu Gln Ala Gln
1185 1190 1195 1200

Gln Asn Arg Gln Pro Leu Met Asn Gln Ile Ser Asn Val Ser Asn Val
1205 1210 1215

Asn Leu Thr Leu Arg Pro Gly Val Pro Thr Gln Ala Pro Ile Asn Ala
1220 1225 1230

Gln Met Leu Ala Gln Arg Gln Arg Glu Ile Leu Asn Gln His Leu Arg
1235 1240 1245

Gln Arg Gln Met His Gln Gln Gln Gln Val Gln Gln Arg Thr Leu Met
1250 1255 1260

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[illegible]

Ala His Gly Val Ala Arg Ser Ser Thr Leu Pro Pro Ser Asn Ser Asn
20 25 30

Met Val Ser Thr Arg Ile Asn Arg Gln Gln Ser Ser Asp Leu His Ser
35 40 45

Ser Ser His Ser Asn Ser Ser Asn Ser Gln Gly Ser Phe Gly Cys Ser
50 55 60

Pro Gly Ser Gln Ile Val Ala Asn Val Ala Leu Asn Lys Gly Gln Ala
65 70 75 80

Ser Ser Gln Ser Ser Lys Pro Ser Leu Asn Leu Asn Asn Pro Pro Met
85 90 95

Glu Gly Thr Gly Ile Ser Leu Ala Gln Phe Met Ser Pro Arg Arg Gln
100 105 110

Val Thr Ser Gly Leu Ala Thr Arg Pro Arg Met Pro Asn Asn Ser Phe
115 120 125

Pro Pro Asn Ile Ser Thr Leu Ser Ser Pro Val Gly Met Thr Ser Ser
130 135 140

Ala Cys Asn Asn Asn Asn Arg Ser Tyr Ser Asn Ile Pro Val Thr Ser
145 150 155 160

Leu Gln Gly Met Asn Glu Gly Pro Asn Asn Ser Val Gly Phe Ser Ala
165 170 175

Ser Ser Pro Val Leu Arg Gln Met Ser Ser Gln Asn Ser Pro Ser Arg
180 185 190

Leu Asn Ile Gln Pro Ala Lys Ala Glu Ser Lys Asp Asn Lys Glu Ile
195 200 205

Ala Ser Thr Leu Asn Glu Met Ile Gln Ser Asp Asn Ser Ser Ser Asp
210 215 220

Gly Lys Pro Leu Asp Ser Gly Leu Leu His Asn Asn Asp Arg Leu Ser
225 230 235 240

Asp Gly Asp Ser Lys Tyr Ser Gln Thr Ser His Lys Leu Val Gln Leu
245 250 255

Leu Thr Thr Thr Ala Glu Gln Gln Leu Arg His Ala Asp Ile Asp Thr
260 265 270

Ser Cys Lys Asp Val Leu Ser Cys Thr Gly Thr Ser Asn Ser Ala Ser
275 280 285

Ala Asn Ser Ser Gly Gly Ser Cys Pro Ser Ser His Ser Ser Leu Thr
290 295 300

Ala Arg His Lys Ile Leu His Arg Leu Leu Gln Glu Gly Ser Pro Ser
305 310 315 320

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Asp Ile Thr Thr Leu Ser Val Glu Pro Asp Lys Lys Asp Ser Ala Ser
 325 330 335
 Thr Ser Val Ser Val Thr Gly Gln Val Gln Gly Asn Ser Ser Ile Lys
 340 345 350
 Leu Glu Leu Asp Ala Ser Lys Lys Lys Glu Ser Lys Asp His Gln Leu
 355 360 365
 Leu Arg Tyr Leu Leu Asp Lys Asp Glu Lys Asp Leu Arg Ser Thr Pro
 370 375 380
 Asn Leu Ser Leu Asp Asp Val Lys Val Lys Val Glu Lys Lys Glu Gln
 385 390 395 400
 Met Asp Pro Cys Asn Thr Asn Pro Thr Pro Met Thr Lys Ala Thr Pro
 405 410 415
 Glu Glu Ile Lys Leu Glu Ala Gln Ser Gln Phe Thr Ala Asp Leu Asp
 420 425 430
 Gln Phe Asp Gln Leu Leu Pro Thr Leu Glu Lys Ala Ala Gln Leu Pro
 435 440 445
 Gly Leu Cys Glu Thr Asp Arg Met Asp Gly Ala Val Thr Ser Val Thr
 450 455 460
 Ile Lys Ser Glu Ile Thr Ile Lys Ser Glu Ile Leu Pro Ala Ser Leu
 465 470 475 480
 Gln Ser Ala Thr Ala Arg Pro Thr Ser Arg Leu Asn Arg Leu Pro Glu
 485 490 495
 Leu Glu Leu Glu Ala Ile Asp Asn Gln Phe Gly Gln Pro Gly Thr Gly
 500 505 510
 Asp Gln Ile Pro Trp Thr Asn Asn Thr Val Thr Ala Ile Asn Gln Ser
 515 520 525
 Lys Ser Glu Asp Gln Cys Ile Ser Ser Gln Leu Asp Glu Leu Leu Cys
 530 535 540
 Pro Pro Thr Thr Val Glu Gly Arg Asn Asp Glu Lys Ala Leu Leu Glu
 545 550 555 560
 Gln Leu Val Ser Phe Leu Ser Gly Lys Asp Glu Thr Glu Leu Ala Glu
 565 570 575
 Leu Asp Arg Ala Leu Gly Ile Asp Lys Leu Val Gln Gly Gly Gly Leu
 580 585 590
 Asp Val Leu Ser Glu Arg Phe Pro Pro Gln Gln Ala Thr Pro Pro Leu
 595 600 605
 Ile Met Glu Glu Arg Pro Asn Leu Tyr Ser Gln Pro Tyr Ser Ser Pro
 610 615 620

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Phe Pro Thr Ala Asn Leu Pro Ser Pro Phe Gln Gly Met Val Arg Gln
625 630 635 640

Lys Pro Ser Leu Gly Thr Met Pro Val Gln Val Thr Pro Pro Arg Gly
645 650 655

Ala Phe Ser Pro Gly Met Gly Met Gln Pro Arg Gln Thr Leu Asn Arg
660 665 670

Pro Pro Ala Ala Pro Asn Gln Leu Arg Leu Gln Leu Gln Gln Arg Leu
675 680 685

Gln Gly Gln Gln Gln Leu Ile His Gln Asn Arg Gln Ala Ile Leu Asn
690 695 700

Gln Phe Ala Ala Thr Ala Pro Val Gly Ile Asn Met Arg Ser Gly Met
705 710 715 720

Gln Gln Gln Ile Thr Pro Gln Pro Pro Leu Asn Ala Gln Met Leu Ala
725 730 735

Gln Arg Gln Arg Glu Leu Tyr Ser Gln Gln His Arg Gln Arg Gln Leu
740 745 750

Ile Gln Gln Gln Arg Ala Met Leu Met Arg Gln Gln Ser Phe Gly Asn
755 760 765

Asn Leu Pro Pro Ser Ser Gly Leu Pro Val Gln Thr Gly Asn Pro Arg
770 775 780

Leu Pro Gln Gly Ala Pro Gln Gln Phe Pro Tyr Pro Pro Asn Tyr Gly
785 790 795 800

Thr Asn Pro Gly Thr Pro Pro Ala Ser Thr Ser Pro Phe Ser Gln Leu
805 810 815

Ala Ala Asn Pro Glu Ala Ser Leu Ala Asn Arg Asn Ser Met Val Ser
820 825 830

Arg Gly Met Thr Gly Asn Ile Gly Gly Gln Phe Gly Thr Gly Ile Asn
835 840 845

Pro Gln Met Gln Gln Asn Val Phe Gln Tyr Pro Gly Ala Gly Met Val
850 855 860

Pro Gln Gly Glu Ala Asn Phe Ala Pro Ser Leu Ser Pro Gly Ser Ser
865 870 875 880

Met Val Pro Met Pro Ile Pro Pro Pro Gln Ser Ser Leu Leu Gln Gln
885 890 895

Thr Pro Pro Ala Ser Gly Tyr Gln Ser Pro Asp Met Lys Ala Trp Gln
900 905 910

Gln Gly Ala Ile Gly Asn Asn Asn Val Phe Ser Gln Ala Val Gln Asn
915 920 925

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Gln	Pro	Thr	Pro	Ala	Gln	Pro	Gly	Val	Tyr	Asn	Asn	Met	Ser	Ile	Thr
930						935					940				
Val	Ser	Met	Ala	Gly	Gly	Asn	Thr	Asn	Val	Gln	Asn	Met	Asn	Pro	Met
945					950					955					960
Met	Ala	Gln	Met	Gln	Met	Ser	Ser	Leu	Gln	Met	Pro	Gly	Met	Asn	Thr
				965					970					975	
Val	Cys	Pro	Glu	Gln	Ile	Asn	Asp	Pro	Ala	Leu	Arg	His	Thr	Gly	Leu
			980					985					990		
Tyr	Cys	Asn	Gln	Leu	Ser	Ser	Thr	Asp	Leu	Leu	Lys	Thr	Glu	Ala	Asp
		995					1000					1005			
Gly	Thr	Gln	Gln	Val	Gln	Gln	Val	Gln	Val	Phe	Ala	Asp	Val	Gln	Cys
1010						1015					1020				
Thr	Val	Asn	Leu	Val	Gly	Gly	Asp	Pro	Tyr	Leu	Asn				
1025					1030					1035					

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu	Arg	Ala	Asp	Gly	Gln	Ser	Arg	Leu	His	Asp	Ser	Lys	Gly	Gln	Thr
1				5				10					15		
Lys	Leu	Leu	Gln	Cys											
			20												

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Gly His Lys Lys Leu Leu Gln Leu Leu Thr Cys Ser Ser His Gly Ser
1 5 10 15
Leu Leu Gln Glu Lys His Arg Ile Leu His Lys Leu Leu Gln Asn Gly
20 25 30
Asn Asn Ala Leu Leu Arg Tyr Leu Leu Asp Arg Asp Asp Pro Ser Asp
35 40 45

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Ser Ile Leu Thr Ser Leu Leu Leu Asn Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Phe Asn Val Leu Lys Gln Leu Leu Leu Ser Glu Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Ala Thr Leu Arg Ser Leu Leu Leu Asn Pro His
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Arg Asn Ser Leu Asp Asp Leu Leu Gly Pro Pro Ser Asn Ala Glu
1 5 10 15

Gly Gln Ser Asp Glu Arg Ala Leu Leu Asp Gln Leu His Thr Phe Leu
20 25 30

Ser Asn Thr Asp Ala Thr Gly Leu Glu Glu Ile Asp Arg Ala Leu Gly
35 40 45

Ile Pro Glu Leu Val Asn Gln Gly Gln Ala
50 55

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGACCTGTTG AACTTTGCAA AGGCAAGGGC AGTTCCTTTG AGCTGGGCTT ATGACCTTTG 60
ACTC 64

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGGAGGACAG TCCTCCGGCG GCCGCGGTCA CAGTGACC

38

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Xaa Xaa Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Xaa Xaa Leu Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Leu Xaa Xaa Leu Xaa Xaa Xaa Leu
1 5

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